

KHINTCHINE-POLLACZEK FORMULA FOR RANDOM WALKS WHOSE STEPS HAVE ONE GEOMETRIC TAIL

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ABSTRACT. We derive a Khintchine-Pollaczek formula for random walks whose steps have a geometric left tail. The construction rests on the memory-less property of the geometric distribution. An example from a tandem queue modeling dynamic instability in microtubules is given.

1. INTRODUCTION

Many results in queueing theory are based on the connection of the waiting times process and an associated random walk. If the queue is an $M/M/1$ queue, then a classical result for the associated random walk is the Khintchine-Pollaczek formula, [4, XII.5]. The derivation exploits the “memoryless” property of the exponential distribution. In this paper we obtain a discrete version of this result, using the memoryless property of the geometric distribution. The discreteness of the distribution introduces a number of additional subtleties, but in general our proof is organized as the proof of the continuous case in [2].

The motivation to consider the discrete case came from our attempt to model what is known as “dynamic instability” of microtubules (see [1, Ch. 16]) by a tandem queue. While the primary queue of the tandem is $M/M/1$, the secondary queue is not. However, the primary queue bequeathes a geometric left tail to the secondary queue and this caused us to search for a Khintchine-Pollaczek formula in that setting.

2. PRELIMINARIES

Let X_1, X_2, \dots , be a sequence of independent random variables with common distribution F not concentrated on a half-axis. The *induced*

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random walk is the sequence of random variables

$$S_0 = 0, \quad S_n = X_1 + \cdots + X_n.$$

The integer n is a (strict) ladder index for the random walk if

$$\max_{0 \leq k < n} S_k < S_n.$$

If n is a ladder index, then S_n is the *ladder height* associated with n . For Borel sets $A \subset (0, \infty)$, define a finite measure L by

$$(1) \quad L(A) = \sum_{n=1}^{\infty} P \left(\max_{0 \leq k < n} S_k = 0 < S_n \in A \right).$$

The probability that there is at least one ladder index is

$$(2) \quad p = L(0, \infty) = P \left(\sup_n S_n > 0 \right).$$

Let T_1 be the first ladder index, and denote H_1 the first ladder height, i.e. $H_1 = S_{T_1}$. These variables are defective with probability $1 - p$ and remain undefined if there is no first ladder index. In fact, for $x > 0$,

$$(3) \quad L[x, \infty) = P(H_1 \geq x).$$

Following the notation in [4, Chapter XII], we call the smallest n such that $S_1 < 0, \dots, S_{n-1} < 0$, but $S_n \geq 0$ the *first weak ladder index* and denote it by \bar{T}_1 . The corresponding *weak ladder height* is denoted by \bar{H}_1 , so that $\bar{H}_1 = S_{\bar{T}_1}$. Again, these variables are possibly defective. We set

$$(4) \quad \zeta = P(\bar{H}_1 = 0) = \sum_{n=1}^{\infty} P \left(\max_{1 \leq k < n} S_k < 0, S_n = 0 \right).$$

Since $X_1 > 0$ implies $\bar{H}_1 > 0$ and it is assumed that X_1 is not concentrated on a half-axis, it follows that $0 \leq \zeta < 1$.

Lemma 1. *For $x > 0$, we have*

$$(5) \quad P(\bar{T}_1 < T_1, H_1 \geq x) = \zeta P(H_1 \geq x).$$

Proof. If $0 < k < n$ and $P(\bar{T}_1 = k, \bar{H}_1 = 0) > 0$, then

$$P(T_1 = n, H_1 \geq x | \bar{T}_1 = k, \bar{H}_1 = 0) = P(T_1 = n - k, H_1 \geq x)$$

by the Markov property. Thus

$$\begin{aligned}
& P(\bar{T}_1 < T_1, H_1 \geq x) \\
&= \sum_{n=2}^{\infty} \sum_{k=1}^{n-1} P(\bar{T}_1 = k, T_1 = n, H_1 \geq x) \\
&= \sum_{k=1}^{\infty} \sum_{n=k+1}^{\infty} P(\bar{T}_1 = k, \bar{H}_1 = 0) P(T_1 = n, H_1 \geq x | \bar{T}_1 = k, \bar{H}_1 = 0) \\
(6) \quad &= \sum_{k=1}^{\infty} P(\bar{T}_1 = k, \bar{H}_1 = 0) \sum_{n=1}^{\infty} P(T_1 = n, H_1 \geq x).
\end{aligned}$$

□

Denote L^{n*} the n -fold convolution of L with itself and L^{0*} a unit mass at the point 0. Define the measure ψ by

$$(7) \quad \psi(A) = \sum_{n=0}^{\infty} L^{n*}(A), \quad A \subset [0, \infty).$$

We have, cf. [2, Theorem 24.2(iii)],

Theorem 2. *If $p < 1$, then with probability $p^n(1-p)$ there are exactly n ladder indices; with probability 1 there are only finitely many ladder indices and $\sup_n S_n < \infty$; finally*

$$(8) \quad P\left(\sup_{n \geq 0} S_n \in A\right) = (1-p)\psi(A), \quad A \subset [0, \infty).$$

Furthermore, cf. [2, Theorem 24.3],

Theorem 3. *The measure ψ satisfies*

$$(9) \quad \int_{y \leq x} \psi[0, x-y] dF(y) = \sum_{n=1}^{\infty} P\left(\min_{1 \leq k < n} S_k > 0, S_n \leq x\right).$$

3. ONE-SIDED GEOMETRIC TAILS

We assume from now on that the random variables X_i are integer valued.

Theorem 4 (Geometric right tail). *Suppose that $\mathbb{E}[X_1] < 0$ and that the right tail of F is geometric:*

$$(10) \quad P(X_1 \geq x) = \xi r^x, \quad x = 0, 1, \dots,$$

where $0 < \xi < 1$ and $0 < r < 1$. Then $p < 1$ and

$$(11) \quad P\left(\sup_{n \geq 0} S_n > x\right) = p [1 - (1-p)(1-r)]^x, \quad x = 0, 1, \dots$$

Moreover, $1/[1 - (1-p)(1-r)]$ is the unique root of the equation

$$(12) \quad \sum_{x=-\infty}^{\infty} s^x P(X_1 = x) = 1$$

in the range $1 < s < 1/r$.

Proof. For $x \geq 0$ we have

$$(13) \quad P\left(\max_{0 \leq k < n} S_k \leq 0, S_n > x\right) = P\left(S_n > x | S_n > 0, \max_{0 \leq k < n} S_k \leq 0\right) P\left(\max_{0 \leq k < n} S_k \leq 0, S_n > 0\right),$$

and also

$$(14) \quad \begin{aligned} & P\left(S_n > x | S_n > 0, \max_{0 \leq k < n} S_k \leq 0\right) \\ & = P\left(X_n > x - S_{n-1} | X_n > -S_{n-1}, \max_{0 \leq k < n} S_k \leq 0\right). \end{aligned}$$

Furthermore, since X_n is independent of S_0, \dots, S_{n-1} , and the geometric distribution is *memoryless*,

$$(15) \quad \begin{aligned} & P\left(X_n > x - S_{n-1} | X_n > -S_{n-1}, \max_{0 \leq k < n} S_k \leq 0\right) \\ & = \frac{1}{\xi} P(X_n \geq x) = r^x. \end{aligned}$$

Whence

$$(16) \quad P\left(\max_{0 \leq k < n} S_k \leq 0, S_n > x\right) = r^x P\left(\max_{0 \leq k < n} S_k \leq 0 < S_n\right),$$

and so

$$(17) \quad \begin{aligned} L((x, \infty)) &= \sum_{n=1}^{\infty} P\left(\max_{0 \leq k < n} S_k \leq 0, S_n > x\right) \\ &= r^x \sum_{n=1}^{\infty} P\left(\max_{0 \leq k < n} S_k \leq 0 < S_n\right) = r^x p. \end{aligned}$$

This shows that the measure L is p times the geometric distribution with parameter $1 - r$. Hence L^{n*} is p^n times the negative binomial distribution with parameters n and $1 - r$: For $x > 0$,

$$L^{n*}\{x\} = \begin{cases} p^n \binom{x-1}{n-1} (1-r)^n r^{x-n}, & \text{if } 1 \leq n \leq x; \\ 0, & \text{otherwise.} \end{cases}$$

In particular, for $x = 1, 2, \dots$,

$$\psi\{x\} = \sum_{n=1}^x p^n \binom{x-1}{n-1} (1-r)^n r^{x-n} = p(1-r)[1 - (1-p)(1-r)]^{x-1},$$

so that

$$\begin{aligned} \psi([0, x]) &= 1 + \sum_{k=1}^x p(1-r)[1 - (1-p)(1-r)]^{k-1} \\ (18) \quad &= \begin{cases} 1 + (1-r)x, & \text{if } p = 1; \\ \frac{1}{1-p} - \frac{p}{1-p} [1 - (1-p)(1-r)]^x, & \text{if } p < 1. \end{cases} \end{aligned}$$

Since $\mathbb{E}[X_1] < 0$, we have $S_n \rightarrow -\infty$ P -a.s and $p < 1$. The identity (11) now follows from (8).

Next, since $S_n \rightarrow -\infty$, the right side of (9) is equal to one for $x = 0$, so that by (18)

$$(19) \quad \sum_{y=-\infty}^0 (1 - p[1 - (1-p)(1-r)]^{-y}) F\{y\} = 1 - p.$$

Denote $f(s)$ the probability generating function of X_1 given on the left in (12). Because of (10), it is defined for $0 \leq s < 1/r$ and

$$f(s) = \sum_{y=-\infty}^{-1} s^y F\{y\} + \frac{\xi(1-r)}{1 - rs}.$$

Since $1 < 1/[1 - (1-p)(1-r)] < 1/r$, it follows from this, (19), and $F(-1) = 1 - \xi$, that $f(1/[1 - (1-p)(1-r)]) = 1$.

Finally, $f(1) = 1$ and, since $P(X_1 < 0) > 0$,

$$f''(s) = \sum_{\mathbb{Z} \setminus \{0,1\}} x(x-1)s^{x-2} F\{x\} > 0$$

for $0 < s < 1/r$. Hence equation (12) cannot have more than one root in $(1, 1/r)$. □

Theorem 5 (Geometric left tail). *Suppose that $\mathbb{E}[X_1] < 0$ and that the left tail of F is geometric:*

$$(20) \quad P(X_1 \leq x) = \xi r^{-x}, \quad x = 0, -1, \dots,$$

where $0 < \xi < 1$ and $0 < r < 1$. Then

$$(21) \quad (1 - \zeta)p = r + (1 - r)\mathbb{E}[X_1],$$

and for $x = 1, 2, \dots$,

$$(22) \quad (1 - \zeta)L(0, x] = F(x) - F(0) + (1 - r) \sum_{m=1}^x (1 - F(m)).$$

Proof. Assume first not (20) but (10), and assume also that $\mathbb{E}[X_1] > 0$. In that case, $S_n \rightarrow \infty$, P -a.s., so that $p = 1$ by (2). Thus, from (18), we have $\psi[0, x] = 1 + (1 - r)x$ for $x \geq 0$. Whence, for $x \geq 0$ (cf. (9)),

$$\begin{aligned} & \sum_{n=1}^{\infty} P \left(\min_{1 \leq k \leq n} S_k > 0, S_n \leq x \right) \\ &= \sum_{m \leq x} [1 + (1 - r)(x - m)] P(X_1 = m) \\ (23) \quad &= [1 + (1 - r)x] P(X_1 \leq x) - (1 - r) \sum_{m \leq x} m P(X_1 = m). \end{aligned}$$

If (20) holds with $\mathbb{E}[X_1] < 0$, then the above applies to the sequence $\{-X_n\}$. In particular, if X_n is replaced by $-X_n$, x by $-x$, then (23) becomes

$$\begin{aligned} & \sum_{n=1}^{\infty} P \left(\max_{1 \leq k \leq n} S_k < 0, S_n \geq x \right) \\ (24) \quad &= [1 - (1 - r)x] P(X_1 \geq x) + (1 - r) \sum_{m \geq x} m P(X_1 = m). \end{aligned}$$

Recall the definitions of the weak/strict first ladder index. We have for $x > 0$

$$\begin{aligned} & P \left(\max_{0 \leq k \leq n} S_k = 0 < S_n, S_n \geq x \right) - P \left(\max_{1 \leq k \leq n} S_k < 0, S_n \geq x \right) \\ (25) \quad &= P(\bar{T}_1 < T_1 = n, S_n \geq x). \end{aligned}$$

Thus, from (5) and (3),

$$\begin{aligned}
 L[x, \infty) &= \sum_{n=1}^{\infty} P \left(\max_{1 \leq k \leq n} S_k < 0, S_n \geq x \right) + \sum_{n=1}^{\infty} P \left(\overline{T}_1 < T_1 = n, S_n \geq x \right) \\
 (26) \quad &= \sum_{n=1}^{\infty} P \left(\max_{1 \leq k \leq n} S_k < 0, S_n \geq x \right) + \zeta L[x, \infty).
 \end{aligned}$$

Since

$$\sum_{m \geq x} m P(X_1 = m) = x P(X_1 \geq x) + \sum_{m \geq x} (1 - F(m)),$$

it follows from (24) and (26) that

$$(27) \quad (1 - \zeta) L[x, \infty) = 1 - F(x - 1) + (1 - r) \sum_{m \geq x} (1 - F(m)).$$

From (20),

$$(28) \quad \sum_{m \leq 0} m P(X_1 = m) = -\xi r (1 - r) \sum_{m \geq 1} m r^{m-1} = -\xi \frac{r}{1 - r}.$$

Using $F(0) = \xi$, this gives

$$(29) \quad \sum_{m \geq 0} (1 - F(m)) = \mathbb{E}[X_1] - \sum_{m \leq 0} m P(X_1 = m) = \mathbb{E}[X_1] + \frac{r}{1 - r} F(0).$$

Hence

$$\begin{aligned}
 (1 - \zeta) L[1, \infty) &= 1 - F(0) + (1 - r) \sum_{m \geq 1} (1 - F(m)) \\
 (30) \quad &= r + (1 - r) \mathbb{E}[X_1],
 \end{aligned}$$

from which (21) follows. Applying (30) and (27) to

$$L(0, x] = L[1, \infty) - L[x + 1, \infty)$$

gives (22). \square

Corollary 6 (Khintchine-Pollaczek formula). *Under the assumptions of Theorem 5, if*

$$\mathcal{M}(s) = \mathbb{E} \left[s^{\sup_{n \geq 0} S_n} \right], \quad \mathcal{F}^+(s) = \mathbb{E}[s^{X_1}, X_1 > 0],$$

then

$$(31) \quad \mathcal{M}(s) = \frac{1 - \zeta - r - (1 - r) \mathbb{E}[X_1]}{1 - \zeta - \left[\left(1 - \frac{1-r}{1-s} \right) \mathcal{F}^+(s) + s^{\frac{1-r}{1-s}} (1 - F(0)) \right]}.$$

Proof. It follows from (22) that

$$(1 - \zeta)L\{x\} = P(X_1 = x) + rP(X_1 > x).$$

Thus, if $\mathcal{L}(s) = \mathbb{E}[s^{H_1}, \sup_{n \geq 0} S_n > 0]$, then

$$\begin{aligned} (1 - \zeta)\mathcal{L}(s) &= \sum_{x=1}^{\infty} s^x P(X_1 = x) + (1 - r) \sum_{x=1}^{\infty} s^x \sum_{m=x+1}^{\infty} P(X_1 = m) \\ &= \mathcal{F}^+(s) + (1 - r) \sum_{m=1}^{\infty} P(X_1 = m) \left[\frac{s}{1-s} - \frac{s^m}{1-s} \right] \\ (32) \quad &= \left(1 - \frac{1-r}{1-s} \right) \mathcal{F}^+(s) + s \frac{1-r}{1-s} (1 - F(0)). \end{aligned}$$

From (8) and (7) we see that

$$(33) \quad \mathcal{M}(s) = (1-p) \sum_{n=0}^{\infty} \mathcal{L}^n(s).$$

Using (32) and (21), the result follows. \square

4. AN EXAMPLE FROM QUEUING THEORY

We now apply the above results to a particular distribution F with a geometric left tail. The choice of F is motivated by an application of queueing theory to the dynamics of cellular filaments.

4.1. Nucleotide hydrolysis and cap dynamics: a M/M/1-queue. ATP (GTP)-bound monomers arrive at the + end of an actin or tubulin filament and attach themselves. The filament acts as an ATPase (or GTPase) and hydrolyses the bound ATP to ADP (or GTP to GDP). We assume that hydrolysis is “vectorial,” meaning that monomers are hydrolyzed one after the other and in the order they arrived. Consequently, a filament consists of a hydrolyzed part which includes the minus end of the filament, and an unhydrolyzed part containing the +-end of the filament. The unhydrolyzed part is called the *ATP(GTP)-cap* (or simply *cap*).

The nucleotide-bound monomer at the minus-end of the cap is next to a hydrolyzed monomer. We call this transition the *hydrolysis edge*. Only the nucleotide-bound monomer at the hydrolysis edge undergoes hydrolysis at that time. We model the dynamics of the cap as a single server queue where the nucleotide-bound monomers are the “customers,” the ATP(GTP)-cap is the queue, and the service provided by the “server” at the minus end of the cap is hydrolysis. It is assumed

that monomers arrive individually at times \mathbf{t}_n and that the interarrival times σ_n are independent and identically distributed exponential random variables with parameter $1/\alpha$, so that

$$P\{\sigma_n > t\} = e^{-t/\alpha}, \text{ for } t \geq 0, \text{ and } \mathbb{E}[\sigma_n] = \alpha, \quad n = 1, 2, \dots$$

The service time τ_n is the duration of hydrolysis (from the moment the hydrolysis edge reaches the monomer and hydrolysis commences, until hydrolysis of the monomer is completed) for the n th monomer arriving after $t = 0$. The random variables $\tau_n, n = 1, 2, \dots$, are assumed to be independent, identically distributed exponential random variables with parameter $1/\beta$ and mean $\mathbb{E}[\tau_n] = \beta$. Furthermore, we assume that the families $\{\sigma_n, n \geq 1\}$ and $\{\tau_n, n \geq 1\}$ are independent.

The actual waiting time $\mathbf{w}_n, n = 1, 2, \dots$ is the time from the moment of arrival of the n th monomer until its hydrolysis commences. A busy period is the *lifetime* of an ATP/GTP-cap, and the number of customers present in the system at time t , \mathbf{x}_t , is the length of the ATP/GTP-cap at time t . Hence $\{\mathbf{x}_t = 0\}$ stands for: “at time t the filament is uncapped.” For an introduction to queueing theory, see [3].

4.2. Catastrophe and rescue: a coupled queue. Once filamentous monomers have undergone hydrolysis, they enter a second queue, the hydrolyzed segment of the filament. The n th customer (hydrolyzed monomer) joining this queue after $t = 0$ arrives at time \mathbf{r}_n , the departure time from the first queue (the cap). For this second queue, we assume that the “server” is only active when no cap is present. The “service” consists of dissociation of a monomer from the filament. Service is provided in the inverse order of arrival—“last come, first served.” This service policy means that at the moment the ATP/GTP-cap disappears, hydrolyzed monomers start dissociating from the +-end. Dissociation continues until an ATP(GTP)-bound monomer arrives and “caps” the filament. The service times (dissociation times) ν_n for this second queue are assumed to be independent and identically distributed exponential random variables with parameter $1/\gamma$. The parameter (or rate) $1/\gamma$ is assumed to be much larger than the rate of arrival of ATP(GTP)-bound monomers, $1/\alpha$, so that when the filament is uncapped, it quickly loses monomers—undergoes a “catastrophe”—until it is capped again by an ATP(GTP)-bound monomer—the “rescue.” For an introduction to the dynamics of cellular filaments, see [1, Ch. 16].

Thus a rescue occurs at the beginning of a busy period of the first server, while a catastrophe commences when the busy period ends.

Denote \mathbf{n} the number of monomers added to the second queue during a rescue.

4.3. Results for the ATP(GTP)-cap. Since the cap is modeled as an M/M/1-queue, results are readily available in the literature, [3, II.2]. We assume from now on that $a \equiv \beta/\alpha < 1$, i.e. that the rate at which monomers are hydrolyzed exceeds the rate at which monomers arrive at the +-end of the filament.

- *Cap length.* The cap length \mathbf{x}_t is an ergodic Markov process with stationary distribution

$$(34) \quad u_j = \lim_{t \rightarrow \infty} P\{\mathbf{x}_t = j | \mathbf{x}_0 = k\} = \lim_{t \rightarrow \infty} P\{\mathbf{x}_t = j\} = a^j(1-a),$$

for $j = 0, 1, \dots$. Thus

$$(35) \quad \lim_{t \rightarrow \infty} \mathbb{E}[\mathbf{x}_t] = \frac{a}{1-a}, \quad \lim_{t \rightarrow \infty} \text{Var}[\mathbf{x}_t] = \frac{a^2}{(1-a)^2} + \frac{a}{1-a}.$$

- *Cap lifetime—duration of rescue (busy period).* The cap lifetime ρ has mean

$$(36) \quad \beta/(1-a).$$

- *Monomers hydrolyzed while filament capped.* The probability that while the filament is capped exactly k monomers are hydrolyzed is given by

$$(37) \quad P\{\mathbf{n} = k\} = \frac{1}{2k-1} \binom{2k-1}{k} \frac{a^{k-1}}{(1+a)^{2k-1}}, \quad k = 1, 2, \dots$$

These probabilities have the generating function

$$(38) \quad U(s) = \sum_{k=1}^{\infty} P\{\mathbf{n} = k\} s^k = \frac{1+a}{2a} \left(1 - \sqrt{1 - \frac{4as}{(1+a)^2}} \right),$$

which converges for $|s| < 1 + (1-a)^2/4a$. It follows readily that

$$(39) \quad \mathbb{E}[\mathbf{n}] = \frac{1}{1-a}.$$

- *Maximal cap length.* The probability that during a busy period the maximal cap length does not exceed h monomers is given by

$$(40) \quad \frac{1 - a^h}{1 - a^{h+1}}, \quad h = 1, 2, \dots$$

4.4. The hydrolyzed filament. During a busy period monomers are hydrolyzed (serviced in the M/M/1-queue) and become part of the hydrolyzed part of the filament (“arrive at” the coupled queue). During an idle period of the M/M/1-queue (when the filament is uncapped), hydrolyzed monomers dissociate from the +‐end of the filament. For $k = 1, 2, \dots$, denote \mathbf{n}_k the number of monomers hydrolyzed during the k -th busy period. The variables $\mathbf{n}_k, k = 1, 2, \dots$ are independent and identically distributed with distribution given by (37).

Since the time until the arrival of the next ATP(GTP)-bound monomer is exponential with parameter $1/\alpha$ and the time until dissociation of a hydrolyzed monomer is exponential with parameter $1/\gamma$, we have

$$P\{\text{monomer dissociates before capping monomer arrives}\} = \frac{\alpha}{\alpha + \gamma}.$$

Furthermore, since exponential random variables are memoryless, this implies that

$$\begin{aligned} P\{m \text{ monomers dissociate before filament is capped}\} \\ (41) \quad &= \left(\frac{\alpha}{\alpha + \gamma} \right)^m \frac{\gamma}{\alpha + \gamma}, \quad m = 0, 1, \dots, \end{aligned}$$

assuming that the filament contains at least m monomers.

Denote $\mathbf{z}_k, k = 1, 2, \dots$, the length of the filament at the time of the k -th rescue. If at $t = 0$ the length of the filament is 0, then \mathbf{z}_1 is the number of monomers hydrolyzed during the first busy period minus the number of monomers dissociated during the first idle period, i.e.

$$\mathbf{z}_1 = \max(\mathbf{n}_1 - \mathbf{m}_1, 0),$$

where \mathbf{m}_1 is independent of \mathbf{n}_1 and has distribution given by (41). More generally, it is easily seen that

$$(42) \quad \mathbf{z}_{k+1} = \max(\mathbf{z}_k + \mathbf{n}_{k+1} - \mathbf{m}_{k+1}, 0), \quad k = 0, 1, \dots,$$

where the random variables $\mathbf{m}_k, k = 1, 2, \dots$, are independent and identically distributed with the common distribution (41), and independent of the variables $\mathbf{n}_k, k = 1, 2, \dots$. Thus, from [4, VI.9], we see that the sequence $\mathbf{z}_k, k = 1, 2, \dots$, can be considered the sequence of waiting times for a single server queue, with interarrival times \mathbf{m}_k , and service times $\mathbf{n}_k, k = 1, 2, \dots$. Since neither variable is exponentially distributed, this queue is a G/G/1-queue, for which far fewer explicit results of the type listed above for the M/M/1-queue exist. However, the interarrival times \mathbf{m}_k have a geometric distribution, which is the discrete analogue of the exponential distribution. In particular, the

interarrival time distribution is also memoryless,

$$P\{\mathbf{m}_k \geq m + n | \mathbf{m}_k \geq m\} = P\{\mathbf{m}_k \geq n\},$$

for $m, n = 0, 1, \dots$, and $k = 1, 2, \dots$

Since $\mathbb{E}[\mathbf{n}_k] = \alpha/(\alpha - \beta)$ (cf. (39)), and $\mathbb{E}[\mathbf{m}_k] = \alpha/\gamma$, it follows that the G/G/1-queue has load

$$b = \frac{\gamma}{\alpha - \beta}.$$

We have $b < 1$ if and only if $\beta + \gamma < \alpha$, i.e. if the average time for hydrolysis and dissociation of a monomer is less than the average time between the arrival of ATP(GTP)-bound monomers.

We now apply our random walk results from above. Let

$$X_k = \mathbf{n}_k - \mathbf{m}_k, \quad \text{and} \quad r = \frac{\alpha}{\alpha + \gamma}.$$

Then $b < 1$ implies

$$(43) \quad \frac{1}{1-a} - \frac{r}{1-r} < 0.$$

Furthermore,

$$P(\mathbf{m}_1 \geq k) = r^k.$$

Thus, if V denotes the generating function of \mathbf{m}_1 , then

$$(44) \quad V(s) = \mathbb{E}[s^{\mathbf{m}_1}] = \frac{1-r}{1-rs}, \quad |s| < 1/r.$$

Denote F the common distribution of X_k . Then $F(x) = \xi r^{-x}$, $x = 0, -1, \dots$, with $\xi = U(r)$,

$$\mathbb{E}[X_1] = \mathbb{E}[\mathbf{n}_1] - \mathbb{E}[\mathbf{m}_1] = \frac{1}{1-a} - \frac{r}{1-r} < 0,$$

and

$$r + (1-r)\mathbb{E}[X_1] = \frac{1-r}{1-a}.$$

Moreover,

$$\mathcal{F}^+(s) = V(1/s)[U(s) - U(r)],$$

and

$$\mathcal{M}(s) = \frac{1 - \zeta - \frac{1-r}{1-a}}{1 - \zeta - (1-r)s\frac{1-U(s)}{1-s}}.$$

A series representation for ζ is readily found using Lemma 2 in [4, XVIII.3] and the fact that the constant term in $[U(s)V(1/s)]^n$ equals $P(X_1 + \dots + X_n = 0)$.

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